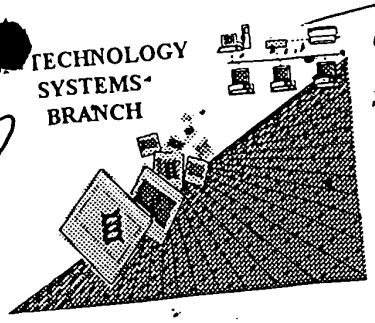
0590 0590 0988

10/23

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/904994

Source: OIPE

Date Processed by STIC: 10/04/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/904994

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PT

1____Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2____Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3____Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4____Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5____Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6____PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7____Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences
8____Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequen <210> sequence id number <400> sequence id number 000
9__✓__Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent
10____Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknow is Artificial Sequence
11____Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules
12____PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13____Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to repres any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001
TIME: 17:34:16

Input Set : A:\20005661.app
Output Set: N:\CRF3\10042001\I904994.raw

Does Not Comply
Corrected Diskette Needed
See Page 6 of 8 A
As well as Error
Summary Sheet

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  3 <110> APPLICANT: KUSTERS, Johannes G.
  4       CATTOLI, Giovanni
  6 <120> TITLE OF INVENTION: HELICOBACTER FELIS VACCINES
  8 <130> FILE REFERENCE: KUSTERS
 10 <140> CURRENT APPLICATION NUMBER: 09/904,994
C--> 11 <141> CURRENT FILING DATE: 2001-09-24
 13 <150> PRIOR APPLICATION NUMBER: EP00202565.8
 14 <151> PRIOR FILING DATE: 2000-07-17
 16 <160> NUMBER OF SEQ ID NOS: 21
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2883
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Helicobacter felis
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 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (206)..(886)
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (897)..(2603)
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 38 ttacttatat taaaaagtta ataaaaagta acgaaattag gactataatc ccattgcctt 180
 40 taaaatttaa cacaaggagt aatag gtg aaa ctc aca ccc aaa gag caa gaa   232
 41                             Val Lys Leu Thr Pro Lys Glu Gln Glu
 42                               1               5
 44 aag ttc ttg tta tat tat gcg ggc gaa gtg gct aga aag cgc aaa gca   280
 45 Lys Phe Leu Leu Tyr Tyr Ala Gly Glu Val Ala Arg Lys Arg Lys Ala
 46  10                  15                  20                  25
 48 gag ggc tta aag ctc aac caa ccc gaa gcc att gct tac att agt gcc   328
 49 Glu Gly Leu Lys Leu Asn Gln Pro Glu Ala Ile Ala Tyr Ile Ser Ala
 50                  30                  35                  40
 52 cat att atg gac gaa gcg cgc cgt gga aaa aaa acc gtt gcc cag ctt   376
 53 His Ile Met Asp Glu Ala Arg Arg Gly Lys Lys Thr Val Ala Gln Leu
 54              45                  50                  55
 56 atg gaa gag tgc atg cac ttt ttg aaa aaa gat gaa gta atg ccc ggg   424
 57 Met Glu Glu Cys Met His Phe Leu Lys Lys Asp Glu Val Met Pro Gly
 58          60                  65                  70
 60 gtg ggt aat atg gtt ccc gat cta ggt gta gaa gcc acc ttt cct gat   472
 61 Val Gly Asn Met Val Pro Asp Leu Gly Val Glu Ala Thr Phe Pro Asp
 62      75                  80                  85
 64 ggt acg aaa ctt gta act gtg aat tgg ccc atc gaa cca gat gag cac   520
 65 Gly Thr Lys Leu Val Thr Val Asn Trp Pro Ile Glu Pro Asp Glu His
 66  90                  95                  100                 105
 68 ttc aaa gcg ggc gaa gtg aaa ttt ggt tgc gat aaa gac atc gag ctc   568
 69 Phe Lys Ala Gly Glu Val Lys Phe Gly Cys Asp Lys Asp Ile Glu Leu
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RAW SEQUENCE LISTING DATE: 10/04/2001
PATENT APPLICATION: US/09/904,994 TIME: 17:34:16

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Output Set: N:\CRF3\10042001\I904994.raw

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     70                 110                 115                 120
     72 aat gca ggc aaa gaa gta acc gaa ctt gag gtt act aat gaa ggg cct   616
     73 Asn Ala Gly Lys Glu Val Thr Glu Leu Glu Val Thr Asn Glu Gly Pro
     74             125                 130                 135
     76 aaa tcc ttg cat gtg ggt agc cat ttc cac ttc ttt gaa gct aac aag   664
     77 Lys Ser Leu His Val Gly Ser His Phe His Phe Phe Glu Ala Asn Lys
     78         140                 145                 150
     80 gca cta aaa ttc gat cgt gaa aaa gcc tat ggc aaa cgc cta gat att   712
     81 Ala Leu Lys Phe Asp Arg Glu Lys Ala Tyr Gly Lys Arg Leu Asp Ile
     82     155                 160                 165
     84 ccc tct ggc aac acg cta cgc att ggg gca gga caa acc cgc aaa gtg   760
     85 Pro Ser Gly Asn Thr Leu Arg Ile Gly Ala Gly Gln Thr Arg Lys Val
     86 170                 175                 180                 185
     88 cag ttg att cct ctt ggt ggc agt aaa aaa gtg att ggc atg aac ggg   808
     89 Gln Leu Ile Pro Leu Gly Gly Ser Lys Lys Val Ile Gly Met Asn Gly
     90                 190                 195                 200
     92 ctt gtg aat aac atc gcg gat gaa cgc cat aaa cat aaa gcg ctt gac   856
     93 Leu Val Asn Asn Ile Ala Asp Glu Arg His Lys His Lys Ala Leu Asp
     94             205                 210                 215
     96 aag gcg aaa tct cac gga ttt atc aag taa ggagactccc atg aaa atg    905
     97 Lys Ala Lys Ser His Gly Phe Ile Lys                Met Lys Met
W--> 98         220                 225                     230
    100 aaa aaa caa gaa tat gta aat acc tac gga ccc acc aaa ggc gat aaa   953
    101 Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Lys Gly Asp Lys
W--> 102                235                 240                 245
    104 gtg cgc tta gga gat acc gat ctt tgg gca gaa gta gaa cat gac tat  1001
    105 Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu His Asp Tyr
W--> 106            250                 255                 260
    108 acc acc tat ggc gaa gaa ctt aaa ttt ggc gcg ggt aaa act atc cgt  1049
    109 Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys Thr Ile Arg
W--> 110         265                 270                 275
    112 gag ggt atg ggt cag agc aat agc cct gat gaa aac acc cta gat tta  1097
    113 Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr Leu Asp Leu
W--> 114     280                 285                 290
    116 gtc atc act aac gcg atg att atc gac tac acc ggg att tac aaa gcc  1145
    117 Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile Tyr Lys Ala
W--> 118 295                 300                 305                 310
    120 gac att ggg att aaa aac ggc aaa atc cat ggc att ggc aag gca gga  1193
    121 Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly Lys Ala Gly
W--> 122                315                 320                 325
    124 aac aag gac atg caa gat ggc gta agc cct cat atg gtc gtg ggt gtg  1241
    125 Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val Val Gly Val
W--> 126            330                 335                 340
    128 ggc aca gaa gca cta gca ggg gaa ggt atg att att acc gct ggg gga  1289
    129 Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr Ala Gly Gly
W--> 130         345                 350                 355
    132 atc gat tca cac acc cac ttc ctt tct cca caa caa ttc cct acc gct  1337
    133 Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe Pro Thr Ala
W--> 134     360                 365                 370
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RAW SEQUENCE LISTING DATE: 10/04/2001
PATENT APPLICATION: US/09/904,994 TIME: 17:34:16

Input Set : A:\20005661.app
Output Set: N:\CRF3\10042001\I904994.raw

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     136 cta gcc aat ggc gtt aca acc atg ttt gga ggc ggc aca ggt cct gta   1385
     137 Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr Gly Pro Val
W--> 138 375                 380                 385                 390
     140 gat ggc acg aat gcg act act atc act ccg ggc aaa tgg aac ttg cac   1433
     141 Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp Asn Leu His
W--> 142                 395                 400                 405
     144 cgc atg ttg cgc gca gca gaa gag tat tct atg aat gtg ggc ttt ttg   1481
     145 Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val Gly Phe Leu
W--> 146             410                 415                 420
     148 ggc aaa ggc aat agc tct agc aaa aaa caa ctt gta gaa caa gta gaa   1529
     149 Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu Gln Val Glu
W--> 150         425                 430                 435
     152 gcg ggc gcg att ggt ttt aaa ttg cat gaa gac tgg ggc aca aca cca   1577
     153 Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly Thr Thr Pro
W--> 154     440                 445                 450
     156 agt gcg atc gat cac tgc ttg agc gtg gca gat gaa tac gat gtg caa   1625
     157 Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr Asp Val Gln
W--> 158 455                 460                 465                 470
     160 gtt tgt atc cac acc gat aca gtc aat gag gca ggt tat gta gat gac   1673
     161 Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr Val Asp Asp
W--> 162                 475                 480                 485
     164 acc cta aat gca atg aac ggg cgc gcc atc cat gcc tac cac att gag   1721
     165 Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr His Ile Glu
W--> 166             490                 495                 500
     168 gga gcg ggt gga gga cac tca cct gat gtt atc acc atg gca ggc gag   1769
     169 Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met Ala Gly Glu
W--> 170         505                 510                 515
     172 ctc aat att cta ccc tcc tcc acc acc ccc act att ccc tat acc att   1817
     173 Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro Tyr Thr Ile
W--> 174     520                 525                 530
     176 aat acg gtt gca gaa cac tta gac atg ctc atg aca tgc cac cac cta   1865
     177 Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys His His Leu
W--> 178 535                 540                 545                 550
     180 gac aaa cgc atc cgc gag gat tta caa ttt tct caa agc cgt atc cgc   1913
     181 Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser Arg Ile Arg
W--> 182                 555                 560                 565
     184 ccc ggc tct atc gcg gct gaa gat gtg ctc cat gat atg ggt gtg atc   1961
     185 Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Met Gly Val Ile
W--> 186             570                 575                 580
     188 gcg atg aca agc tcg gat tcg caa gca atg ggg cgt gca ggc gaa gtg   2009
     189 Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala Gly Glu Val
W--> 190         585                 590                 595
     192 att cct cga act tgg cag act gcg gat aag aat aaa aaa gaa ttt ggt   2057
     193 Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys Glu Phe Gly
W--> 194     600                 605                 610
     196 aag ctt cct gaa gat ggc aaa gat aac gat aat ttc cgc att aag cgc   2105
     197 Lys Leu Pro Glu Asp Gly Lys Asp Asn Asp Asn Phe Arg Ile Lys Arg
W--> 198 615                 620                 625                 630
     200 tac atc tcc aaa tac act atc aac ccc gct ttg acc cac ggc gtg agc   2153
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001
TIME: 17:34:16

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Output Set: N:\CRF3\10042001\I904994.raw

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W--> 202                 635                 640                 645
     204 gag tat atc ggc tct gtg gaa gag ggc aag atc gcc gac ttg gtg gtg   2201
     205 Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp Leu Val Val
W--> 206             650                 655                 660
     208 tgg aat cct gcc ttt ttt ggc gta aaa ccc aaa atc gtg atc aaa ggc   2249
     209 Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val Ile Lys Gly
W--> 210         665                 670                 675
     212 ggt atg gtg gtc ttc tct gaa atg ggc gat tct aac gcg tct gtg ccc   2297
     213 Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala Ser Val Pro
W--> 214     680                 685                 690
     216 act ccc caa ccg gtt tat tac cgc gaa atg ttt ggg cat cac ggc aag   2345
     217 Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His His Gly Lys
W--> 218 695                 700                 705                 710
     220 gcg aaa ttt gac acc agc atc act ttt gtt tcc aaa gtc gcc tat gaa   2393
     221 Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val Ala Tyr Glu
W--> 222                 715                 720                 725
     224 aat ggc gtg aaa gaa aag ctg ggc tta gag cgc caa gtt cta ccg gtc   2441
     225 Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Gln Val Leu Pro Val
W--> 226             730                 735                 740
     228 aaa aac tgc cgt aac atc acc aag aaa gac ttc aag ttc aac gac aaa   2489
     229 Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe Asn Asp Lys
W--> 230         745                 750                 755
     232 acg gca aaa atc acc gtc gat ccg aaa acc ttc gag gtc ttt gta gat   2537
     233 Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val Phe Val Asp
W--> 234     760                 765                 770
     236 ggc aaa ctc tgc acc tct aaa ccc acc tcg caa gtg cct cta gcc cag   2585
     237 Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser Gln Val Pro Leu Ala Gln
W--> 238 775                 780                 785                 790
     240 cgc tac act ttc ttc tag gcacaatgcc ccctttgggg gcaggttatt         2633
     241 Arg Tyr Thr Phe Phe
W--> 242                 795
     244 ttaggaatct tcatcaaacg cacctgcaat cggtcttgcg tgtgcgatcg tgtcgcttta 2693
     246 aaacaacttt tcatctttaa gcaatcgcca tttttaatta atttaattct tataattaat 2753
     248 attatattat gccccctcat ttttaaagga gaattatgcg taggtctttg gtattgctat 2813
     250 gtgggggttg tttggtgctg ggcgcaaagg gtattgaaac ccatcgcctc aaaaaagtag 2873
     252 aagccacagg                                                       2883
     255 <210> SEQ ID NO: 2
     256 <211> LENGTH: 226
     257 <212> TYPE: PRT
     258 <213> ORGANISM: Helicobacter felis
     260 <400> SEQUENCE: 2
     261 Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
     262   1               5                  10                  15
     263 Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
     264              20                  25                  30
     265 Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
     266          35                  40                  45
     267 Arg Gly Lys Lys Thr Val Ala Gln Leu Met Glu Glu Cys Met His Phe
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RAW SEQUENCE LISTING DATE: 10/04/2001
PATENT APPLICATION: US/09/904,994 TIME: 17:34:16

Input Set : A:\20005661.app
Output Set: N:\CRF3\10042001\I904994.raw

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268      50                  55                  60
269 Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
270  65                  70                  75                  80
271 Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
272                  85                  90                  95
273 Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
274             100                 105                 110
275 Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
276         115                 120                 125
277 Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
278     130                 135                 140
279 His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
280 145                 150                 155                 160
281 Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
282                 165                 170                 175
283 Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
284             180                 185                 190
285 Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
286         195                 200                 205
287 Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
288     210                 215                 220
289 Ile Lys
290 225
293 <210> SEQ ID NO: 3
294 <211> LENGTH: 568
295 <212> TYPE: PRT
296 <213> ORGANISM: Helicobacter felis
298 <400> SEQUENCE: 3
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300   1               5                  10                  15
301 Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu
302              20                  25                  30
303 His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
304          35                  40                  45
305 Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
306      50                  55                  60
307 Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
308  65                  70                  75                  80
309 Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
310                  85                  90                  95
311 Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
312             100                 105                 110
313 Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
314         115                 120                 125
315 Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
316     130                 135                 140
317 Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr
318 145                 150                 155                 160
319 Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
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<211> 2407
<212> DNA
<213> Helicobacter felis

<220>
<221> CDS
<222> (2)..(682)

<220>
<221> CDS
<222> (693)..(2399)

<400> 10

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Pro Ala Ser Glu Val Pro Leu Ala Gln Arg Tyr Thr Phe Phe
            785                 790                 795

gcncaatg                                                          2407
```

<210> 11
<211> 226
<212> PRT
<213> Helicobacter felis

Errored: As you can see sequence 10 includes sequence 10 includes unknown nucleotides. It is required that you describe unknowns in fields 221, 221 and 223.

The type of errors shown may exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001
TIME: 17:34:17

Input Set : A:\20005661.app
Output Set: N:\CRF3\10042001\I904994.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:194 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:202 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:214 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:242 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:446 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:462 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:466 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:470 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:474 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:478 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001
TIME: 17:34:17

Input Set : A:\20005661.app
Output Set: N:\CRF3\10042001\I904994.raw

L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:490 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:1232 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:1232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10